Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 16:06:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080685.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR3080685 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080685.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 16:06:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080685.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,156,003
Mapped reads	1,069,047 / 92.48%
Unmapped reads	86,956 / 7.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,628 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	32,487 / 2.81%
Duplication rate	2.69%
Clipped reads	449,825 / 38.91%

2.2. ACGT Content

Number/percentage of A's	19,853,372 / 27.65%
Number/percentage of C's	13,200,437 / 18.38%
Number/percentage of T's	22,829,858 / 31.79%
Number/percentage of G's	15,925,041 / 22.18%
Number/percentage of N's	3,278 / 0%
GC Percentage	40.56%

2.3. Coverage

Mean	0.0232

Standard Deviation	0.1926

2.4. Mapping Quality

Mean Mapping Quality	46.3

2.5. Mismatches and indels

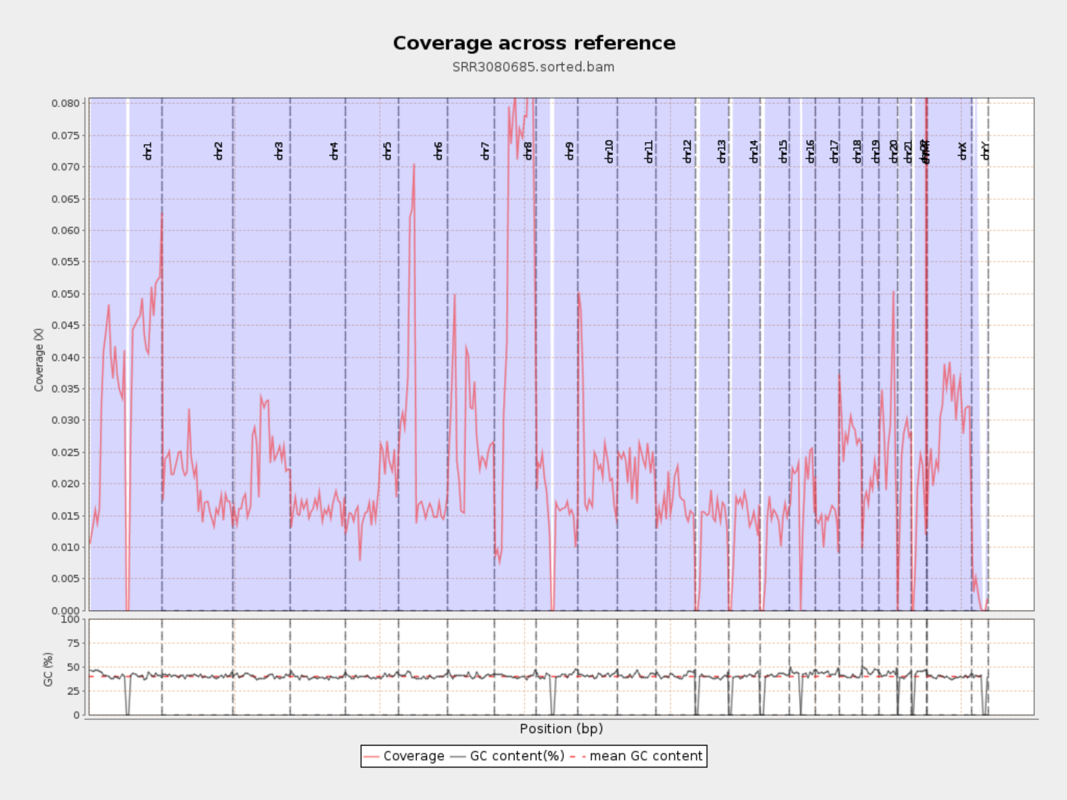
General error rate	0.69%
Mismatches	482,986
Insertions	5,435
Mapped reads with at least one insertion	0.5%
Deletions	16,730
Mapped reads with at least one deletion	1.55%
Homopolymer indels	48.67%

2.6. Chromosome stats

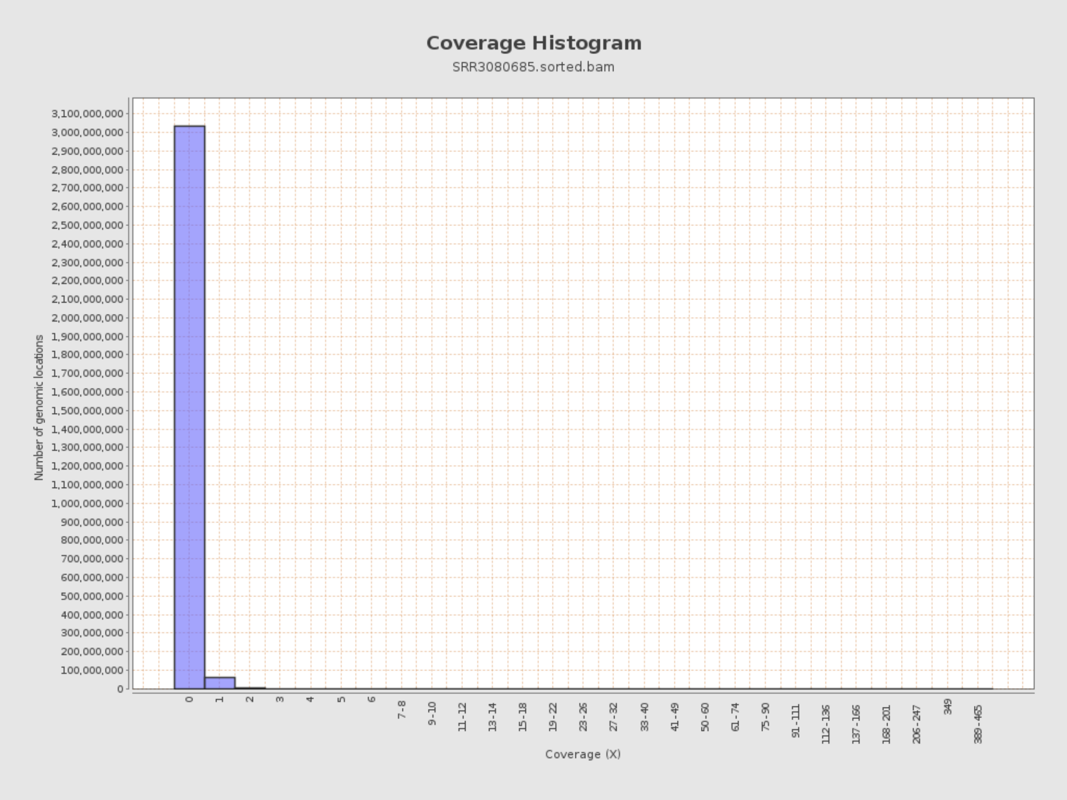
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8925762	0.0358	0.2317
chr2	243199373	4802369	0.0197	0.2529
chr3	198022430	4573982	0.0231	0.1661
chr4	191154276	3097189	0.0162	0.1415
chr5	180915260	3247530	0.018	0.1466
chr6	171115067	4386134	0.0256	0.1988
chr7	159138663	4555437	0.0286	0.2999

chr8	146364022	8545814	0.0584	0.2933
chr9	141213431	2179761	0.0154	0.1472
chr10	135534747	3309216	0.0244	0.1757
chr11	135006516	3116212	0.0231	0.1781
chr12	133851895	2248312	0.0168	0.1411
chr13	115169878	1501780	0.013	0.1245
chr14	107349540	1405702	0.0131	0.1249
chr15	102531392	1236834	0.0121	0.1267
chr16	90354753	1742233	0.0193	0.1532
chr17	81195210	1147814	0.0141	0.1318
chr18	78077248	2205914	0.0283	0.2165
chr19	59128983	1129982	0.0191	0.1641
chr20	63025520	1843110	0.0292	0.1893
chr21	48129895	1093814	0.0227	0.1663
chr22	51304566	724286	0.0141	0.1297
chrMT	16571	20656	1.2465	1.2362
chrX	155270560	4668620	0.0301	0.1951
chrY	59373566	130667	0.0022	0.0529

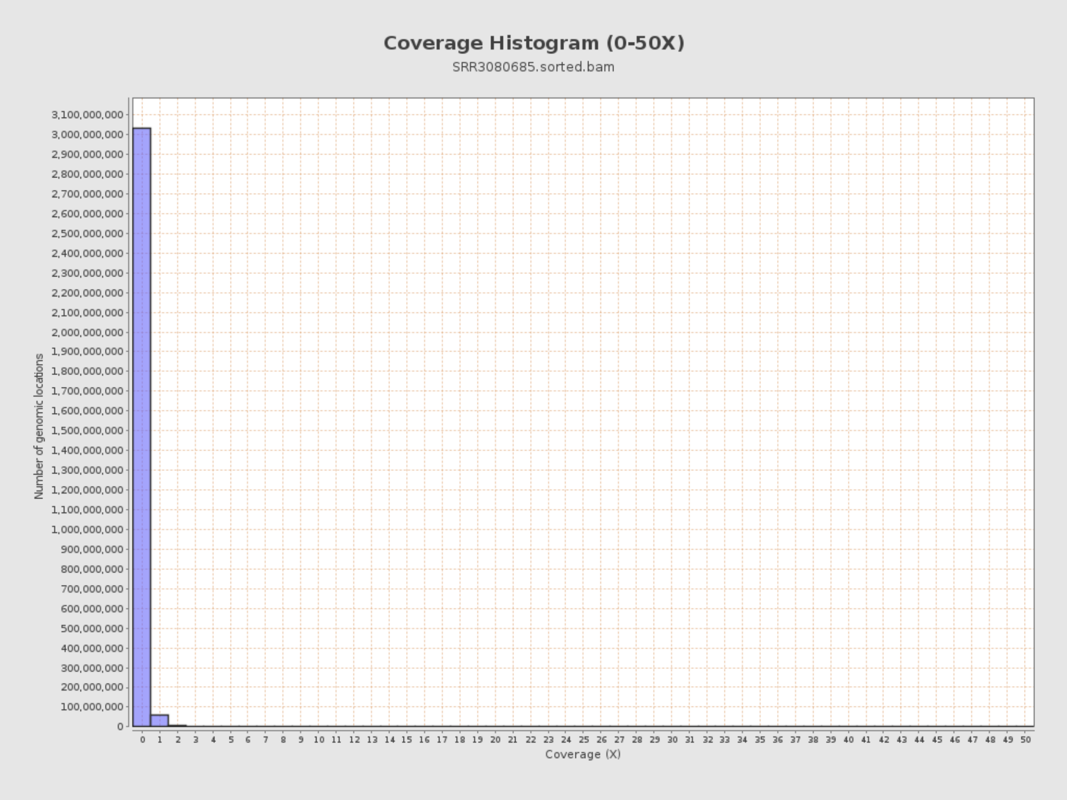
3. Results : Coverage across reference



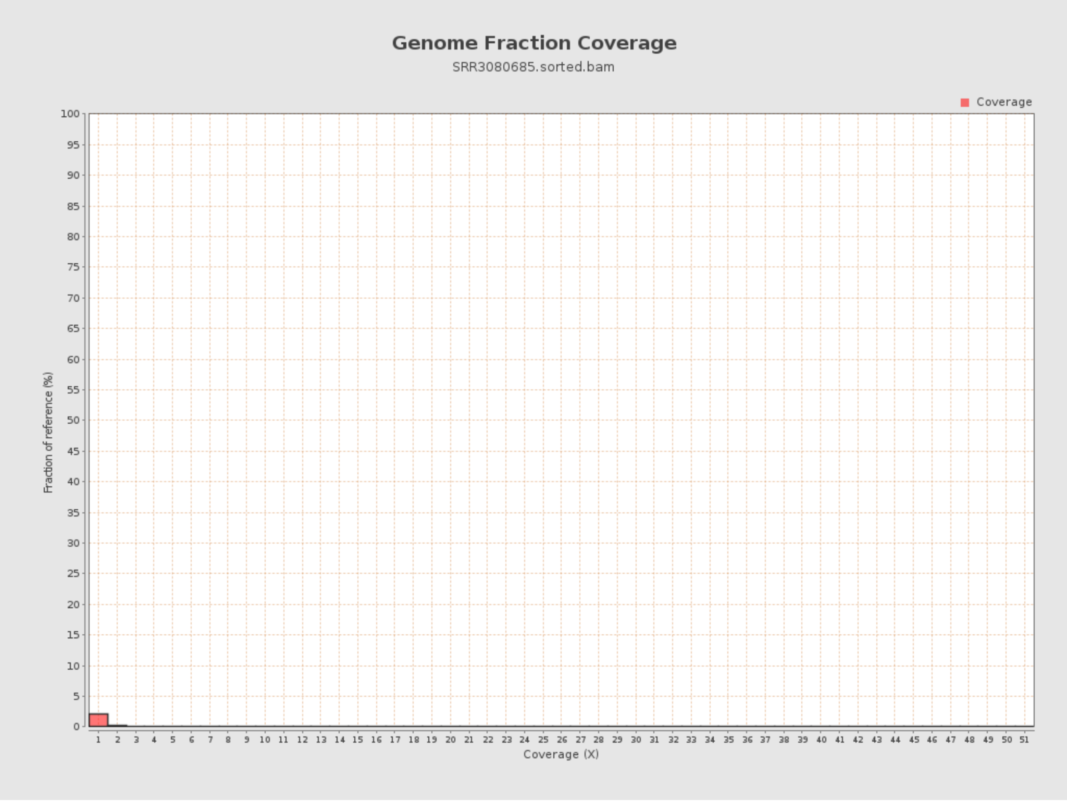
4. Results : Coverage Histogram



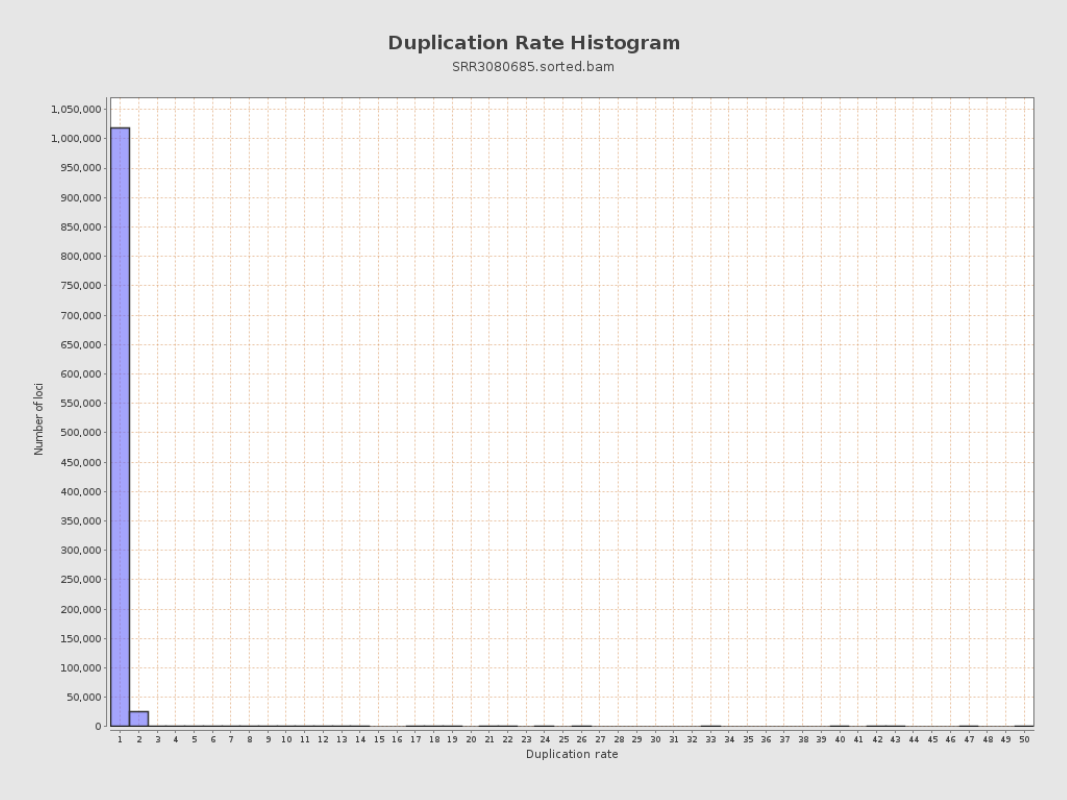
5. Results : Coverage Histogram (0-50X)



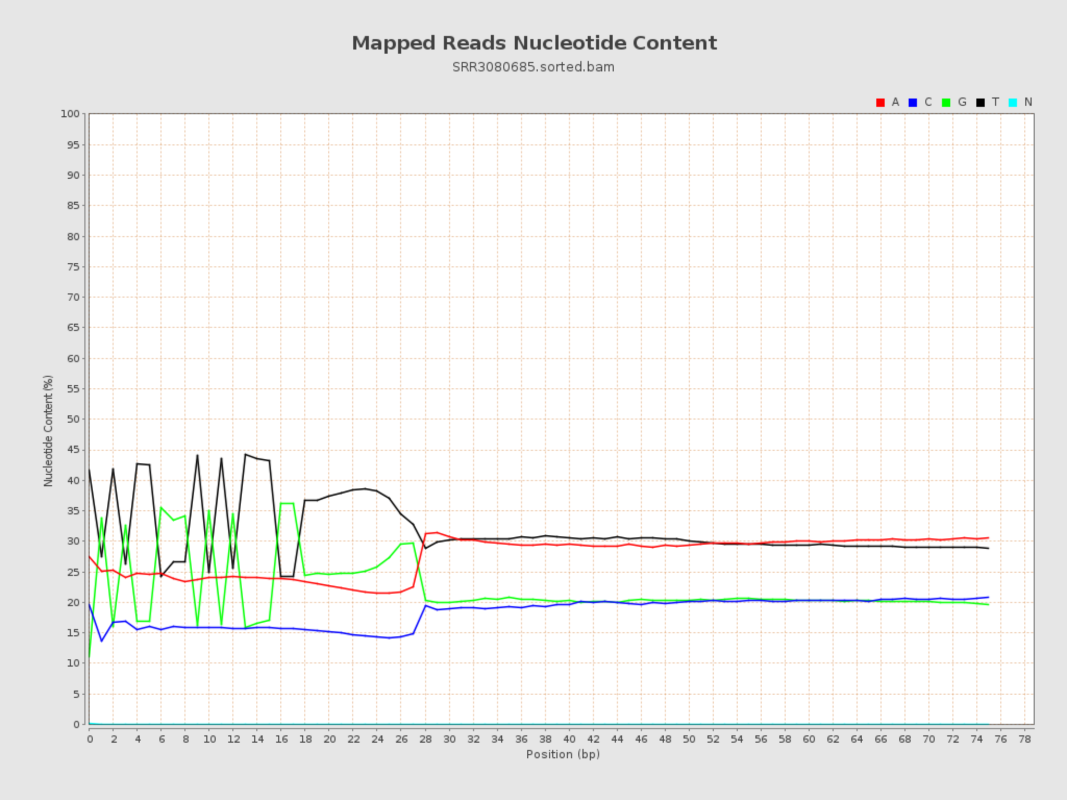
6. Results : Genome Fraction Coverage



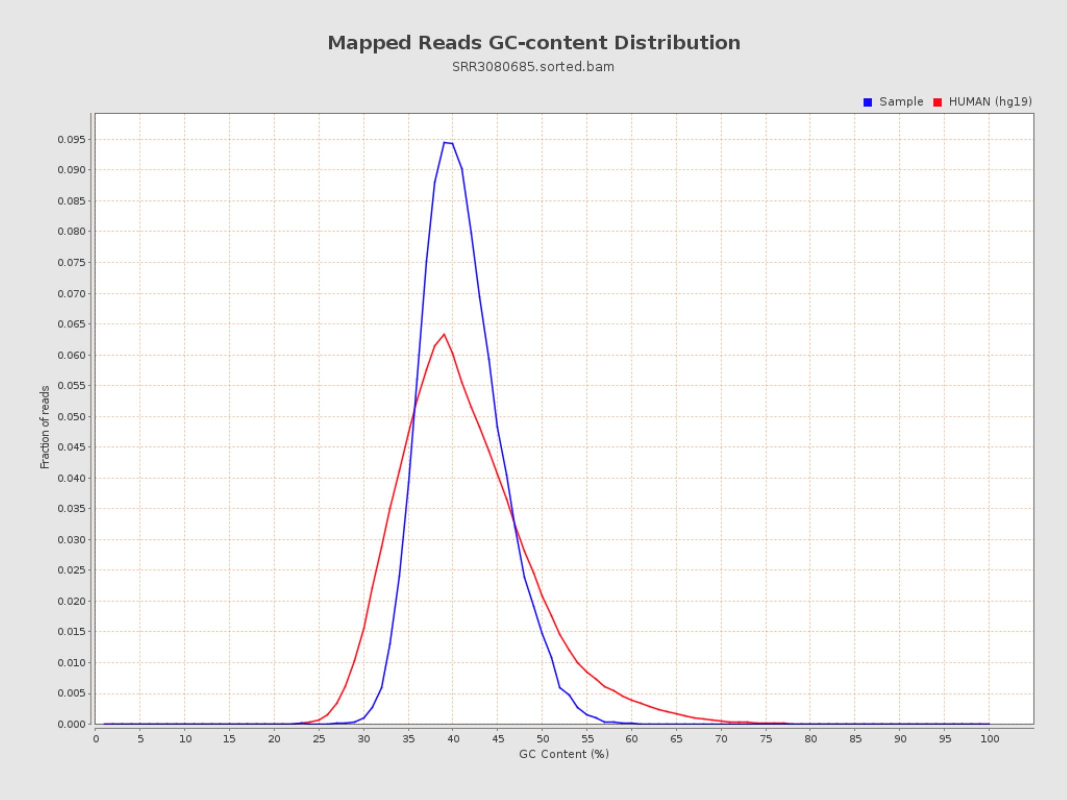
7. Results : Duplication Rate Histogram



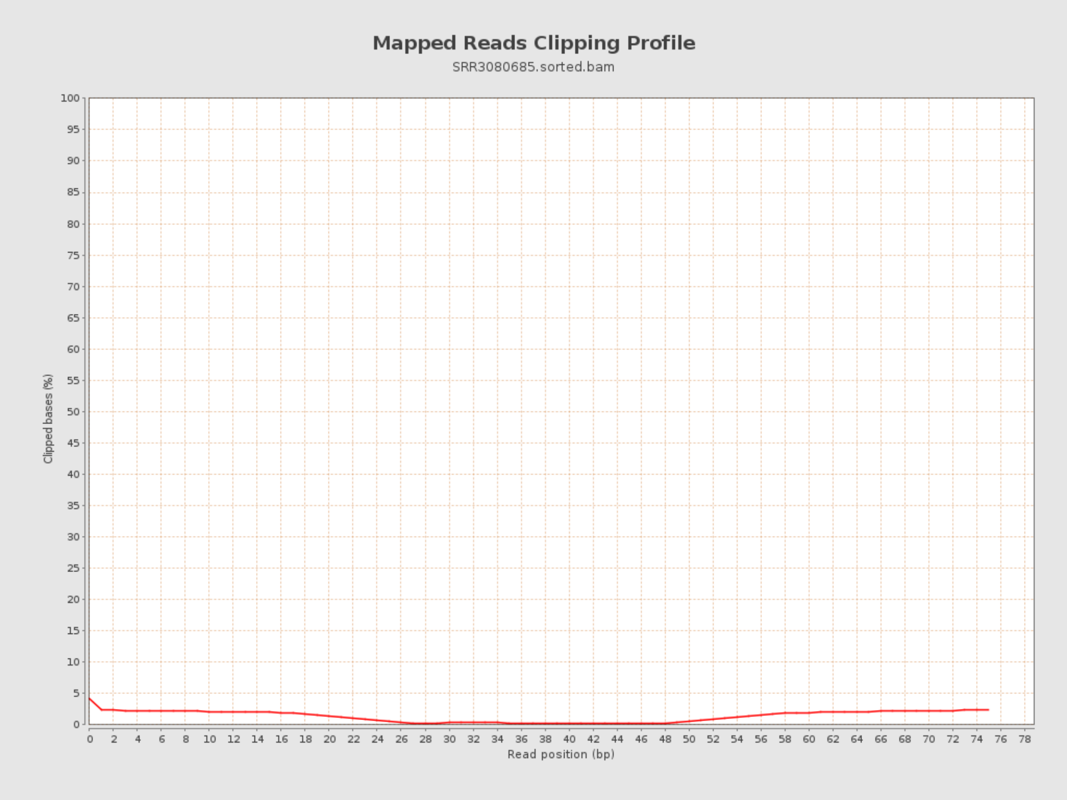
8. Results : Mapped Reads Nucleotide Content



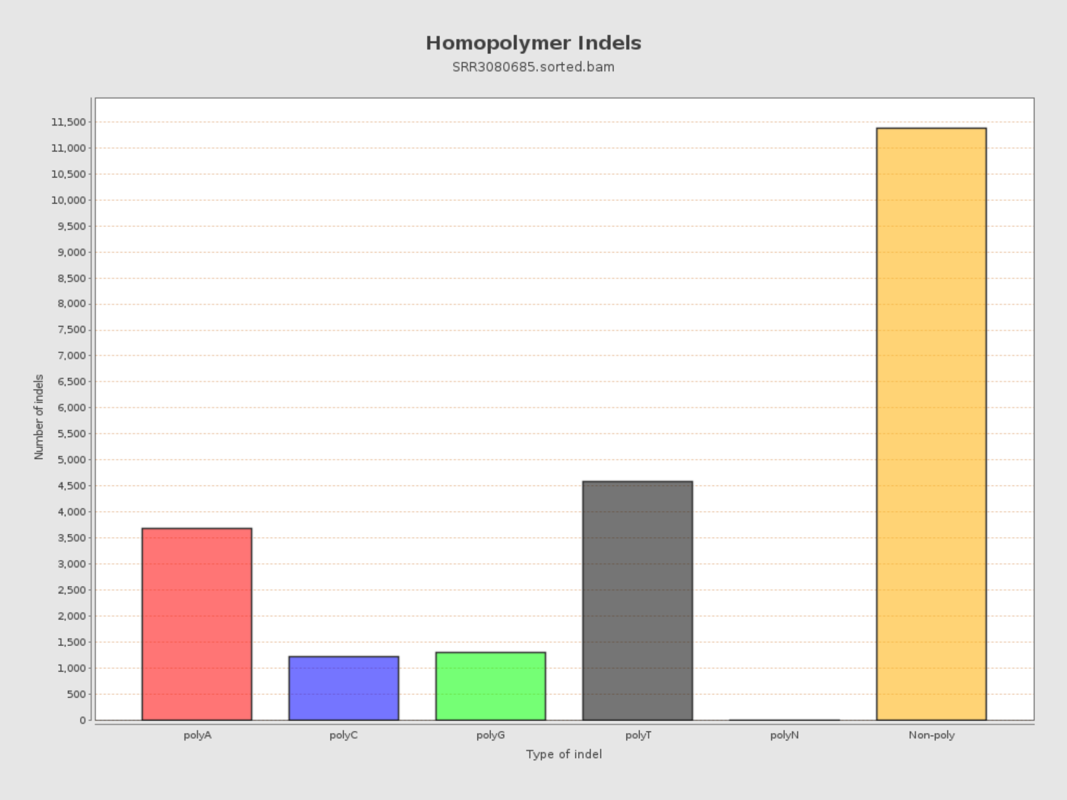
9. Results : Mapped Reads GC-content Distribution



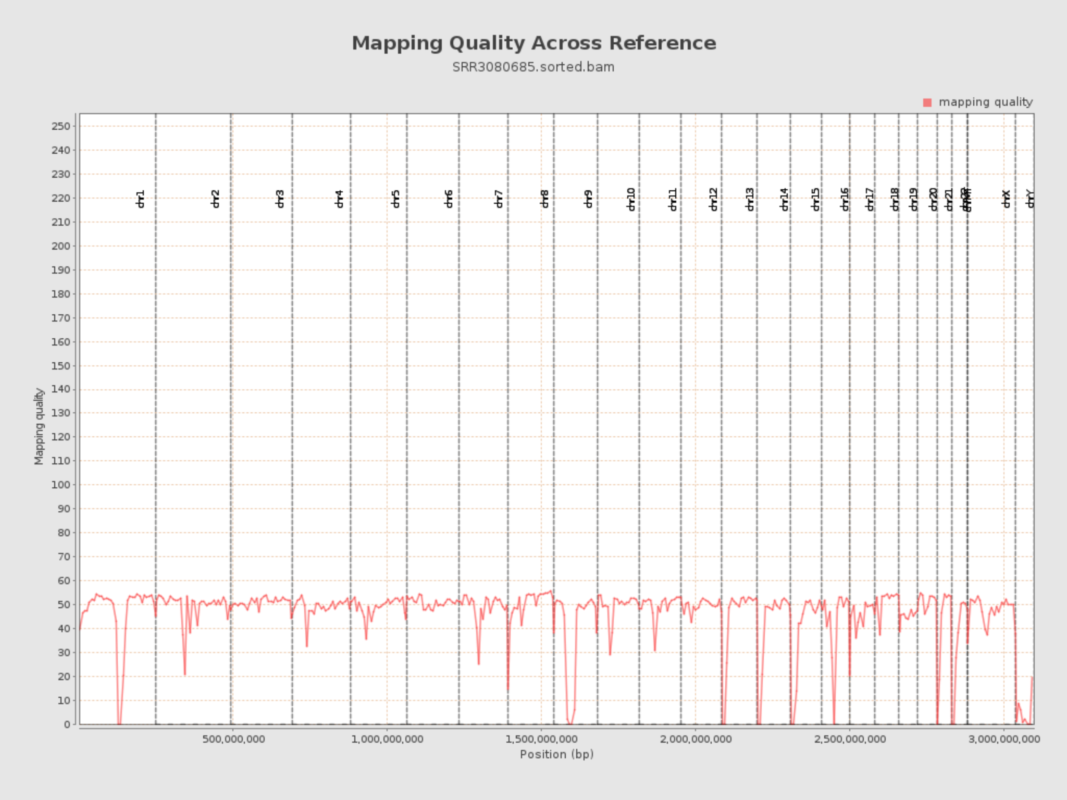
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram